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SEQUENCE LISTING

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D5*

(1) GENERAL INFORMATION:

(i) APPLICANT: Peter Ruhdal Jensen
Karin Hammer

(ii) TITLE OF INVENTION: Artificial promoter libraries
for selected organisms and promoters derived from such
libraries

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/242,657
(B) FILING DATE: February 19, 1999

(vii) PRIOR APPLICATION DATA:

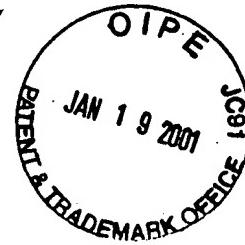
(A) APPLICATION NUMBER: DK 886/96
(B) FILING DATE: 23-AUG-1996
(A) APPLICATION NUMBER: PCT/DK97/00342
(B) FILING DATE: August 25, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) REFERENCE/DOCKET NUMBER: 55411.000002

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:26..82
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

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Cmt
/standard_name= "Artificial promoter library" /note= "A degenerated sequence specifying a mixture of artificial promoters covering a wide range of expression in small steps in L. lactis"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:31..45
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:60..69
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:74..82
- (D) OTHER INFORMATION:/standard_name= "Consensus

sequence"

(ix) FEATURE:

- (A) NAME/KEY: -35_signal
- (B) LOCATION:40..45
- (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:

- (A) NAME/KEY: -10_signal
- (B) LOCATION:63..68
- (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:3..25
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard_name= "Multiple cloning site" /label= MCS
/note= "A sequence specifying recognition sites
for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
MboI,
DpnI, AflII, MseI, SspI, NsiI."

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:74..98
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites
for the restriction endonucleases: ScaI, RsaI, HpaI, HincII,
MseI, SfcI,
PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGATCCTT AAGAATATTA TGCATNNNN AGTTTATTCT TGACANNNN
NNNNNNNNNT 60

GGTATAATAN NANAGTACTG TTAACTGCAG CTGAATTCCG 100

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:23..95
- (D) OTHER INFORMATION:/standard_name=

"Artificial promoter library"

/note= "A degenerated sequence specifying a mixture of artificial temperature regulated promoters covering a wide range of expression in small steps in L. lactis"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:23..49
- (D) OTHER INFORMATION:/standard_name=

"Sequence providing temperature regulation to promoters"

/note= "This sequence comprising two inverted repeats separated by a short spacer provides temperature (heat shock) regulation to promoters in Gram-positive bacteria"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:50..60
- (D) OTHER INFORMATION:/standard_name=

"Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:75..84
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:89..95
(D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:
(A) NAME/KEY: -35_signal
(B) LOCATION:55..60
(D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:
(A) NAME/KEY: -10_signal
(B) LOCATION:78..83
(D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:
(A) NAME/KEY: misc_recomb
(B) LOCATION:3..22
(D) OTHER INFORMATION:/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites
for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
MboI, DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."

(ix) FEATURE:
(A) NAME/KEY: misc_recomb
(B) LOCATION:89..111
(D) OTHER INFORMATION:/standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites
for the restriction endonucleases: ScaI, RsaI, Sfcl, PstI,
Fnu4HI, BbvI,
PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT
TTTTTGACA 60

NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT

CGG

113

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION:10..16
- (D) OTHER INFORMATION:/function= "Activating

promoters in

S. cerevisiae"

/bound_moiety= "GCN4 protein"

/standard_name= "Upstream activating sequence" /label= UAS_GCN4p

/note= "A DNA sequence that specifies a binding site for the GCN4 protein, which activates the transcription of genes involved in amino acid synthesis in S. cerevisiae."

(ix) FEATURE:

- (A) NAME/KEY: TATA_signal
- (B) LOCATION:67..72
- (D) OTHER INFORMATION:/standard_name= "TATA box"

(ix) FEATURE:

- (A) NAME/KEY: misc_signal
- (B) LOCATION:122..144
- (D) OTHER INFORMATION:/function= "Transcription

initiation"
/standard_name= "TI box"

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION:122..144
- (D) OTHER INFORMATION:/bound_moiety= "Arginine repressor"
/standard_name= "arginine repressor binding site"
/label= argR

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION:145..192
- (D) OTHER INFORMATION:/function= "Spacer"
/standard_name= "Part of native sequence for ARG8
gene incl. first codon"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:3..8
- (D) OTHER INFORMATION:/standard_name= "Recognition site for restriction endonuclease EcoRI"
/label= EcoRI_site

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION:192..197
- (D) OTHER INFORMATION:/standard_name= "Recognition site or restriction endonuclease BamHI"
/label= BamHI_site

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:10..192
- (D) OTHER INFORMATION:/standard_name= "Artificial promoter library"
/note= "A degenerated sequence specifying a mixture of
artificial promoters covering a wide range of expression in small steps in S. cerevisiae"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN
NNNNNNNNNN 60

NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN
NNNNNNNNNN
NNNNNNNNNN 120

NCTCTTAAGT GCAAGTGACT GCGAACATT TTTTCGTTG TTAGAATAAT
TCAAGAATCG 180

CTACCAATCA TGGATCCCG
199

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas putida

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:1..45
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard_name= "Artificial promoter library" /note= "A
degenerated sequence specifying a mixture of artificial
promoters covering a wide range of expression in small steps
Pseudomonas putida"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNNTT GRNNNNNNNN NNNNNNNNNN NTATRATNNN NNNNN
45

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

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Cp1*
(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION:/standard_name=
"Constitutional promoter"
/label= Cp1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCTTGA TATAATAAGT
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=
"Constitutional promoter"
/label= Cp12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTAC TTTATTCTTG ACAAAACCAC CAGCTTTGG TATAATACGT
GAGAACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional promoter"

/label= Cp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTGCGCTGG TATAATATAT
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..58

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTGG TATAATAACA
GTACTCAG 58

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..58
- (D) OTHER INFORMATION: /standard_name=
"Constitutional promoter"
/label= Cp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA
GTACTGTT 58

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..58

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA
GTACTGTT 58

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
 - (B) LOCATION: 4..60
 - (D) OTHER INFORMATION: /standard_name=
"Constitutional promoter"
- /label= Cp20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGCAGC CNGGGGCTGA TATCATAGCA
GAGTACTATT 60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTA TCAGGGTTGT ATAATACTAT
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional promoter"

/label= Cp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGTAAG TTTATTCTTC ACACATCTG GGCCCGATGG TATAATAAGT
GAECTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:3..59

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTGCGAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional promoter"

/label= Cp26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT
ATACATGCAT 60

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"
/label= Cp28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..59
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"

/label= Cp29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"
/label= Cp3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"
/label= Cp30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"
/label= Cp32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"

/label= Cp33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

"promoter"
/label= Cp34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..59
- (D) OTHER INFORMATION:/standard_name=

"Constitutional

"promoter"
/label= Cp37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"
/label= Cp38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTGA TATAATACAT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"

/label= Cp39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"

/label= Cp4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG
ATCCTTAAGA 60

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4
- (D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"
/label= Cp40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"

/label= Cp41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT
AAGTACTGTT 60

C1 Cont (2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60
(D) OTHER INFORMATION:/standard_name=
"Constitutional
 promoter"
 /label= Cp42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CATTCGTAAG TITATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT
AACTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..59
- (D) OTHER INFORMATION:/standard_name=
"Constitutional

 promoter"
 /label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TITATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..59
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Constitutional promoter"
/label= Cp5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT
GAGTATGTT 59

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"

/label= Cp6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name=

"Constitutional

promoter"

/label= Cp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT
CTAGATTAGG 60

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"
/label= Cp8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTAG TTTATTCTTG ACAAAACGTAT TGAGGACTGA TATAATAGGT
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard_name=

"Constitutional

promoter"
/label= Cp9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:8..177
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 - /standard_name= "Yeast promoter"
 - /label= Yp102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCTGTA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG
TCCCTTTAT 60

AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT
GCAAGTGACT 120

GCGAACATT TTTTCGTTG TTAGAATAAT TCAAGAATCG CTACCAATCA
TGGATCC
177

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 - /standard_name= "Yeast promoter"

/label= Yp112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCTGATCTCACGGCATCTGATGGTTGACCATAGTCA GGAACATTGT
GCTGGAGTTC 60

CTTGAGGAATGAGTTATAAAAATGGGAGGTTGC GGCTAATGCCAGGCAGGA
GAGGAACCCT 120

CTTAAGTGCAAGTGACTGCA AACATTTTT TCGTTGTTG AATCGCTACC
AATCATGGAT 180

CC
182

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

C
✓
Cont
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: / evidence= EXPERIMENTAL
/ standard_name= "Yeast promoter"
/ label= Yp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAATTCTGTA CTCACTAGGC AGGTACAGTT GGCTCTCGC GGCGCAGGTT
CGTATGCCGC 60

GCCGCCAGGG GCTTTATAAAA GGTCGTCTG GGTACAGTTG GGATGGCTCC
ACGTTTCGGC 120

TCTTAAGTGC AAGTGACTGC GAACATTCG TTTGTTAGAA TAATTCAAGA
ATCGCTACCA 180

ATCATGGATC C
191

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..167
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCTGTA CTCAGGGCCG TACTAAGTAG CTTCGTATG CTATGCGGGG
TTTTATAAAAT 60

CTTGGGCCA TGGTCTGCT GGAAACACC TCTCTTAAGT GCAAGTGACT
GCGAACATT 120

TTTCGTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
167

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..191
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: / evidence= EXPERIMENTAL
/ standard_name= "Yeast promoter"
/ label= Yp154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCTGGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG
GGCGTTCTA 60

GCGCAATCGG GGTATAAAATT TATAAGGAGG CTGCGGGTGC TAGTTGTCT
AGTTGACTC 120

TTAAGTGCAA GTGACTGCGA ACATTTTCG TTTGTTAGAA TAATTCAAGA
ATCGCTACCA 180

ATCATGGATC C

191

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAATTCTGAGCTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG
GAGGTGAGAA 60

GCTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTGGT GGGATAGGGG
GTACTGTACC 120

TCTTAAGTGC AAGTGAUTGC GAACATTTT TTCGTTGTT AGAATAATTG
AAGAATCGCT 180

ACCAATCATG GATCC

195

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..179
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCTGTGA CTCACTAACAG GTTCGCCATT AACAGAACATCG CTGGTAGAAC
ATCGGTAGTT 60

AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT
GCGAGCCTCA 120

ATGCGAACAT TTTTTCTGTT TGTTAGAATA ATTCAAGAAC CGCTACCAAT
CATGGATCC 179

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
 (B) LOCATION: 8..190
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yest promoter"
/label= Yp190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCTGTA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG
CAGGCGAGGG 60

CGGGTGGTTA CGGCTATAAAA TGAGTGTGTTG CAGCCGGTA CGGGCGTACG
AGTAGTGATC 120

TCTTAAATGC AAGTGAUTGC GAACATTTTT TTCGTTGTT AGAATAATTG
AAGAATCGCT 180

ACCAATCATG GATCC

195

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..189

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yest promoter"

/label= Yp191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAATTCTGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA
TTTGAGTG A 60

AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATT
GTTTGGACTC 120

TTAAGTAAAA GTGACTGCGA ACATTTTTT CGTTTGTAG AATAATTCAA
GAATCGCTAC 180

CAATCATGGA TCC
193

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION: 8..166
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GAATTCTGAGCTCACTTAAGGCTACTGCGGAAGTTAGATCTAAGGTCGG
AAATAATTAA 60

GAAAATTACGACATTATAAAA TAGCGGAGAGGCCAGGTGATGGGCACCATT
GTGGGGGGGC 120

TCTTAATTGT TAGAATAATT CAAGAACATCGTACCAATCAT GGATCC
166

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCTGTA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTTAACACCC
CGAATTATAC 60

TCGTCAACTT ATAGTATAAAA CGGAACGCGA CGATACGTT TAGTTTCGG
CGAAGTCGAC 120

TCTTAAGTGC AAGTGACTGC GAACATTTT TTCGTTGTT AGAATAATT
AAGAACGCT 180

ACCAATCATG GATCC
195

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter

- (B) LOCATION:8..183
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/ evidence= EXPERIMENTAL
 - /standard_name= "Yeast promoter"
 - /label= Yp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATTCTGAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG
TCGCGTACTA 60

GTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC
CGCTCTTAAG 120

TGCAAGTGAC TGCGAACATT TTTTCGTTT GTTACAATAA TTCAAGAAC
GCTACCAATC 180

ATGGATCC
188

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/ evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"
/label= Yp435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAATTCTGTA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC
ACGTCTGGAG 60

CAGAGGCTAG ACCTTATAAAA TTATACATGG TGGGAGAGGC GATAGTCTTT
AGAGACGTGC 120

TCTTAAGTGC AAGTGACTGC GAACATTTT TTCGTTGTT AGAATAATT
AAGAACGCT 180

ACCAATCATG GATCC
195

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..184
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAATTCTGTA CTCACAAGAA TGTGGCGGG TCGTTAAACT GAGCCTGGAC
ACCTTGGCTG 60

CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC
CAGCTCTTAA 120

ATGCAAGTGA CTGCGAACAT TTTTCGTT TGTTAGAATA ATTCAAGAAT
CGCTACCAAT 180

CATGGATCC
189

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Saccharomyces cerevisiae

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCTGTA CTCACTCGGA AGATTGGTT TACGATTAGG ATGGCGCGGC

AGAACCGGGG 60

GGGATTCCCT TCTATATAAA GGGTCCGAT ACTACGTGCT GCGGACGGCC
GATCGAGTTA 120

TCTTAAGTGC AAGTGACTGC GAAAATTTT TTCGTTGTT AGAATAATT
AAGAACATCGCT 180

ACCAATCATG GATCC
195

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..171
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAATTCGTGA CTCATCTAGT GAGAGGAGCC GTGGTATCTT GTGTCACCAC
CAGGGGAAAA 60

TAATGGCAGG GGTGTATAAA TGGTCGAGTA GTCGCGACCC ACGCTGCAAG

C¹
Cwcel

GCAAGGAACT 120

CTTAAATTT TTTCGTTGT TAGAATAATT CAAGAATCGC TACCAATCAT
GGATCC

176
